

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/517,645
Source: PCR
Date Processed by STIC: 1/26/06

ENTERED



PCT

RAW SEQUENCE LISTING DATE: 01/26/2006
PATENT APPLICATION: US/10/517,645 TIME: 08:52:28

Input Set : A:\SEQLIST.TXT
Output Set: N:\CRF4\01262006\J517645.raw

4 <110> APPLICANT: Prigent, Claude
 5 Martin, Anne
 7 <120> TITLE OF INVENTION: Anti-Aurora-A Monoclonal Antibody,
 8 Method For Obtaining Same, and Uses Thereof For Diagnosing
 9 and Treating Cancers
 11 <130> FILE REFERENCE: 50376/004001
 13 <140> CURRENT APPLICATION NUMBER: US 10/517,645
 14 <141> CURRENT FILING DATE: 2004-12-10
 16 <150> PRIOR APPLICATION NUMBER: PCT/FR03/01772
 17 <151> PRIOR FILING DATE: 2003-06-12
 19 <150> PRIOR APPLICATION NUMBER: FR 02/07212
 20 <151> PRIOR FILING DATE: 2002-06-12
 22 <160> NUMBER OF SEQ ID NOS: 2
 24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 2253
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Homo sapiens
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (257) ... (1468)
 35 <400> SEQUENCE: 1
 36 ggaagacttg ggtccttggg tcgcaggtgg gagccgacgg gtgggttagac cgtggggat 60
 37 atctcagtgg cggacgagga cggcgggac aaggggcggc tggtcggagt ggcggagcgt 120
 38 caagtccctt gtcggttcct ccgtccctga gtgtcccttgg cgctgccttg tgccgccca 180
 39 ggcctttgc atccgctcct gggcaccgag ggcctgtta gataactgtc tgttacttat 240
 40 tacagctaga ggcattc atg gac cga tct aaa gaa aac tgc att tca gga cct 292
 41 Met Asp Arg Ser Lys Glu Asn Cys Ile Ser Gly Pro
 42 1 5 10
 44 gtt aag gct aca gct cca gtt gga ggt cca aaa cgt gtt ctc gtg act 340
 45 Val Lys Ala Thr Ala Pro Val Gly Gly Pro Lys Arg Val Leu Val Thr
 46 15 20 25
 48 cag caa att cct tgt cag aat cca tta cct gta aat agt ggc cag gct 388
 49 Gln Gln Ile Pro Cys Gln Asn Pro Leu Pro Val Asn Ser Gly Gln Ala
 50 30 35 40
 52 cag cgg gtc ttg tgt cct tca aat tct tcc cag cgc gtt cct ttg caa 436
 53 Gln Arg Val Leu Cys Pro Ser Asn Ser Ser Gln Arg Val Pro Leu Gln
 54 45 50 55 60
 56 gca caa aag ctt gtc tcc agt cac aag ccg gtt cag aat cag aag cag 484
 57 Ala Gln Lys Leu Val Ser Ser His Lys Pro Val Gln Asn Gln Lys Gln
 58 65 70 75
 60 aag caa ttg cag gca acc agt gta cct cat cct gtc tcc agg cca ctg 532
 61 Lys Gln Leu Gln Ala Thr Ser Val Pro His Pro Val Ser Arg Pro Leu

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62	80	85	90	
64	aat aac acc caa aag agc aag cag ccc ctg cca tcg gca cct gaa aat			580
65	Asn Asn Thr Gln Lys Ser Lys Gln Pro Leu Pro Ser Ala Pro Glu Asn			
66	95	100	105	
68	aat cct gag gag gaa ctg gca tca aaa cag aaa aat gaa gaa tca aaa			628
69	Asn Pro Glu Glu Glu Leu Ala Ser Lys Gln Lys Asn Glu Glu Ser Lys			
70	110	115	120	
72	aag agg cag tgg gct ttg gaa gac ttt gaa att ggt cgc cct ctg ggt			676
73	Lys Arg Gln Trp Ala Leu Glu Asp Phe Glu Ile Gly Arg Pro Leu Gly			
74	125	130	135	140
76	aaa gga aag ttt ggt aat gtt tat ttg gca aga gaa aag caa agc aag			724
77	Lys Gly Lys Phe Gly Asn Val Tyr Leu Ala Arg Glu Lys Gln Ser Lys			
78	145	150	155	
80	ttt att ctg gct ctt aaa gtg tta ttt aaa gct cag ctg gag aaa gcc			772
81	Phe Ile Leu Ala Leu Lys Val Leu Phe Lys Ala Gln Leu Glu Lys Ala			
82	160	165	170	
84	gga gtg gag cat cag ctc aga aga gaa gta gaa ata cag tcc cac ctt			820
85	Gly Val Glu His Gln Leu Arg Arg Glu Val Glu Ile Gln Ser His Leu			
86	175	180	185	
88	cgg cat cct aat att ctt aga ctg tat ggt tat ttc cat gat gct acc			868
89	Arg His Pro Asn Ile Leu Arg Leu Tyr Gly Tyr Phe His Asp Ala Thr			
90	190	195	200	
92	aga gtc tac cta att ctg gaa tat gca cca ctt gga aca gtt tat aga			916
93	Arg Val Tyr Leu Ile Leu Glu Tyr Ala Pro Leu Gly Thr Val Tyr Arg			
94	205	210	215	220
96	gaa ctt cag aaa ctt tca aag ttt gat gag cag aga act gct act tat			964
97	Glu Leu Gln Lys Leu Ser Lys Phe Asp Glu Gln Arg Thr Ala Thr Tyr			
98	225	230	235	
100	ata aca gaa ttg gca aat gcc ctg tct tac tgt cat tcg aag aga gtt			1012
101	Ile Thr Glu Leu Ala Asn Ala Leu Ser Tyr Cys His Ser Lys Arg Val			
102	240	245	250	
104	att cat aga gac att aag cca gag aac tta ctt ctt gga tca gct gga			1060
105	Ile His Arg Asp Ile Lys Pro Glu Asn Leu Leu Gly Ser Ala Gly			
106	255	260	265	
108	gag ctt aaa att gca gat ttt ggg tgg tca gta cat gct cca tct tcc			1108
109	Glu Leu Lys Ile Ala Asp Phe Gly Trp Ser Val His Ala Pro Ser Ser			
110	270	275	280	
112	agg agg acc act ctc tgt ggc acc ctg gac tac ctg ccc cct gaa atg			1156
113	Arg Arg Thr Thr Leu Cys Gly Thr Leu Asp Tyr Leu Pro Pro Glu Met			
114	285	290	295	300
116	att gaa ggt cgg atg cat gat gag aag gtg gat ctc tgg agc ctt gga			1204
117	Ile Glu Gly Arg Met His Asp Glu Lys Val Asp Leu Trp Ser Leu Gly			
118	305	310	315	
120	gtt ctt tgc tat gaa ttt tta gtt ggg aag cct cct ttt gag gca aac			1252
121	Val Leu Cys Tyr Glu Phe Leu Val Gly Lys Pro Pro Phe Glu Ala Asn			
122	320	325	330	
124	aca tac caa gag acc tac aaa aga ata tca cgg gtt gaa ttc aca ttc			1300
125	Thr Tyr Gln Glu Thr Tyr Lys Arg Ile Ser Arg Val Glu Phe Thr Phe			
126	335	340	345	

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128 cct gac ttt gta aca gag gga gcc agg gac ctc att tca aga ctg ttg 1348
129 Pro Asp Phe Val Thr Glu Gly Ala Arg Asp Leu Ile Ser Arg Leu Leu
130 350 355 360
132 aag cat aat ccc agc cag agg cca atg ctc aga gaa gta ctt gaa cac 1396
133 Lys His Asn Pro Ser Gln Arg Pro Met Leu Arg Glu Val Leu Glu His
134 365 370 375 380
136 ccc tgg atc aca gca aat tca tca aaa cca tca aat tgc caa aac aaa 1444
137 Pro Trp Ile Thr Ala Asn Ser Ser Lys Pro Ser Asn Cys Gln Asn Lys
138 385 390 395
140 gaa tca gct agc aaa cag tct tag gaatcgtgca gggggagaaa tccttgagcc 1498
141 Glu Ser Ala Ser Lys Gln Ser *
142 400
144 agggctgcca tataacctga caggaacatg ctactgaagt ttattttacc attgactgct 1558
145 gccctcaatc tagaacgcta cacaagaaat atttgttta ctcagcaggt gtgccttaac 1618
146 ctccctattc agaaagctcc acatcaataa acatgacact ctgaagtgaa agtagccacg 1678
147 agaattgtgc tacttatact ggttcataat ctggaggcaa gttcgactg cagccccc 1738
148 gtcagcctgt gctaggcatg gtgttacac aggaggcaaa tccagagcct ggctgtgggg 1798
149 aaagtgacca ctctgccctg accccgatca gttaaaggagc ttttgcataaa ctttcctagt 1858
150 acctgagtga gtgtgttaact tattgggttg gctaaagctgt tggaaatgagt 1918
151 atgtgattct ttttaagtat gaaaataaaag atatatgtac agacttgtat ttttctctg 1978
152 gtggcattcc ttttaggaatg ctgtgtgtct gtccggcacc ccggtaggc tgattgggtt 2038
153 tctagtcctc cttaaccact tatctcccat atgagagtgt gaaaaatagg aacacgtgct 2098
154 ctacccat ttagggattt gcttgggata cagaagaggc catgtgtctc agagctgtta 2158
155 agggcttatt tttttaaaac attggagtca tagcatgtgt gttaaacttta aatatgc 2218
156 taaaataagta tctatgtcta aaaaaaaaaa aaaaaa 2253
158 <210> SEQ ID NO: 2
159 <211> LENGTH: 403
160 <212> TYPE: PRT
161 <213> ORGANISM: Homo sapiens
163 <400> SEQUENCE: 2
164 Met Asp Arg Ser Lys Glu Asn Cys Ile Ser Gly Pro Val Lys Ala Thr
165 1 5 10 15
166 Ala Pro Val Gly Gly Pro Lys Arg Val Leu Val Thr Gln Gln Ile Pro
167 20 25 30
168 Cys Gln Asn Pro Leu Pro Val Asn Ser Gly Gln Ala Gln Arg Val Leu
169 35 40 45
170 Cys Pro Ser Asn Ser Ser Gln Arg Val Pro Leu Gln Ala Gln Lys Leu
171 50 55 60
172 Val Ser Ser His Lys Pro Val Gln Asn Gln Lys Gln Lys Leu Gln
173 65 70 75 80
174 Ala Thr Ser Val Pro His Pro Val Ser Arg Pro Leu Asn Asn Thr Gln
175 85 90 95
176 Lys Ser Lys Gln Pro Leu Pro Ser Ala Pro Glu Asn Asn Pro Glu Glu
177 100 105 110
178 Glu Leu Ala Ser Lys Gln Lys Asn Glu Glu Ser Lys Lys Arg Gln Trp
179 115 120 125
180 Ala Leu Glu Asp Phe Glu Ile Gly Arg Pro Leu Gly Lys Gly Lys Phe
181 130 135 140
182 Gly Asn Val Tyr Leu Ala Arg Glu Lys Gln Ser Lys Phe Ile Leu Ala

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183	145	150	155	160
184	Leu Lys Val Leu Phe Lys Ala Gln Leu Glu Lys Ala Gly Val Glu His			
185		165	170	175
186	Gln Leu Arg Arg Glu Val Glu Ile Gln Ser His Leu Arg His Pro Asn			
187		180	185	190
188	Ile Leu Arg Leu Tyr Gly Tyr Phe His Asp Ala Thr Arg Val Tyr Leu			
189		195	200	205
190	Ile Leu Glu Tyr Ala Pro Leu Gly Thr Val Tyr Arg Glu Leu Gln Lys			
191		210	215	220
192	Leu Ser Lys Phe Asp Glu Gln Arg Thr Ala Thr Tyr Ile Thr Glu Leu			
193		225	230	235
194	240			
195	Ala Asn Ala Leu Ser Tyr Cys His Ser Lys Arg Val Ile His Arg Asp			
196		245	250	255
197	Ile Lys Pro Glu Asn Leu Leu Gly Ser Ala Gly Glu Leu Lys Ile			
198		260	265	270
199	Ala Asp Phe Gly Trp Ser Val His Ala Pro Ser Ser Arg Arg Thr Thr			
200		275	280	285
201	Leu Cys Gly Thr Leu Asp Tyr Leu Pro Pro Glu Met Ile Glu Gly Arg			
202		290	295	300
203	Met His Asp Glu Lys Val Asp Leu Trp Ser Leu Gly Val Leu Cys Tyr			
204		305	310	315
205	320			
206	Glu Phe Leu Val Gly Lys Pro Pro Phe Glu Ala Asn Thr Tyr Gln Glu			
207		325	330	335
208	Thr Tyr Lys Arg Ile Ser Arg Val Glu Phe Thr Phe Pro Asp Phe Val			
209		340	345	350
210	208			
211	Thr Glu Gly Ala Arg Asp Leu Ile Ser Arg Leu Leu Lys His Asn Pro			
212		355	360	365
213	Ser Gln Arg Pro Met Leu Arg Glu Val Leu Glu His Pro Trp Ile Thr			
214		370	375	380
215	385			
216	390	395	400	
217	Lys Gln Ser			

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